Amendments to the Specification

Please replace the paragraph beginning on page 29 with the following amended paragraph:

In one aspect of the invention, methods are provided for using SNP genotyping to identify DNA copy number changes. SNP genotyping can be performed using a number of suitable methods, including genotyping arrays such as the 10K SNP array (Available from Affymetrix, Santa Clara, CA) using the Whole Genome Sampling Assay (WGSA) or other methods of amplification that may or may not involve complexity reduction. Arrays with larger numbers of SNPs may also be used along with any available method of genome amplification. The methods will be described using the Affymetrix 10K SNP array as examples. However, one of skill in the art would appreciate that the methods are not limited to the 10K SNP array. Any array that has perfect match probes that are complementary to regions of the genome may be used. In one embodiment an array is designed to have probe sets comprising perfect match probes for regions that are spread out throughout a genome. For example, the array may have probe ~~probes~~ sets that are spaced approximately 25 bp, 100 bp, 1 kb, 5 kb, 10 kb, or 100 kb apart throughout an entire genome. The array may have probes for a single organism or for two or more organisms. The probe sets may have between 1, 2, 5, 10, 15, 20, 30 or more perfect match probes. Probes may be in probe pairs with a PM and MM probe or the MM probes may [[not]] be left off the array.